

SEQUENCE LISTING

<110> Rapoport, Basil

<120> DISEASE ASSOCIATED HUMAN AUTOANTIBODIES SPECIFIC FOR HUMAN THYROID PEROXIDASE

<130> A1697DIV3

<140> 08/482,402

<141> 1996-06-07

<150> US 08/196,082

<151> 1994-03-03

<150> US 08/182,117

<151> 1994-01-27

<150> PCT/US92/07381

<151> 1992-08-28

<150> PCT/US92/006283

<151> 1992-07-30

<150> US 07/750,579

<151> 1991-08-28

<150> US 07/738,040

<151> 1991-07-30

<150> US 07/559,955

<151> 1990-07-31

<150> US 07/472,070

<151> 1990-01-30

<150> US 07/388,044

<151> 1989-07-31

<160> 12

<170> PatentIn version 3.1

<210> 1

<211> 104

<212> DNA

<213> Homo sapiens

<400> 1

aggctccctc gggtgacttg gatctccatg tcgctggctg ctctgctgat cgaggctccc 60

tcgggtgact tgaattccca tgtagctggc tgctctgctg atcg 104

<210> 2

<211> 3072

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (85)..(2883)

<223>

<400> 2

gaggcaattg aggcgcgccat ttcagaagag ttacagccgt gaaaattact cagcagtgc 60

gttggtctgag aagaggaaaa aaga atg aga gcg ctg gct gtg ctg tct gtc 111
Met Arg Ala Leu Ala Val Leu Ser Val
1 5

acg ctg gtt atg gcc tgc aca gaa gcc ttc ttc ccc ttc atc tcg aga 159
Thr Leu Val Met Ala Cys Thr Glu Ala Phe Phe Pro Phe Ile Ser Arg
10 15 20 25

ggg aaa gaa ctc ctt tgg gga aag cct gag gag tct cgt gtc tct agc 207
Gly Lys Glu Leu Leu Trp Gly Lys Pro Glu Glu Ser Arg Val Ser Ser
30 35 40

gtc ttg gag gaa agc aag cgc ctg gtg gac acc gcc atg tac gcc acg 255
Val Leu Glu Glu Ser Lys Arg Leu Val Asp Thr Ala Met Tyr Ala Thr
45 50 55

atg cag aga aac ctc aag aaa aga gga atc ctt tct gga gct cag ctt 303
Met Gln Arg Asn Leu Lys Lys Arg Gly Ile Leu Ser Gly Ala Gln Leu
60 65 70

ctg tct ttt tcc aaa ctt cct gag cca aca agc gga gtg att gcc cga 351
Leu Ser Phe Ser Lys Leu Pro Glu Pro Thr Ser Gly Val Ile Ala Arg
75 80 85

gca gca gag ata atg gaa aca tca ata caa gcg atg aaa aga aaa gtc 399
Ala Ala Glu Ile Met Glu Thr Ser Ile Gln Ala Met Lys Arg Lys Val
90 95 100 105

aac ctg aaa act caa caa tca cag cat cca acg gat gct tta tca gaa 447
Asn Leu Lys Thr Gln Gln Ser Gln His Pro Thr Asp Ala Leu Ser Glu
110 115 120

gat ctg ctg agc atc att gca aac atg tct gga tgt ctc cct tac atg 495
Asp Leu Leu Ser Ile Ile Ala Asn Met Ser Gly Cys Leu Pro Tyr Met
125 130 135

ctg ccc cca aaa tgc cca aac act tgc ctg gcg aac aaa tac agg ccc 543
Leu Pro Pro Lys Cys Pro Asn Thr Cys Leu Ala Asn Lys Tyr Arg Pro
140 145 150

atc aca gga gct tgc aac aac aga gac cac ccc aga tgg ggc gcc tcc 591
Ile Thr Gly Ala Cys Asn Asn Arg Asp His Pro Arg Trp Gly Ala Ser
155 160 165

aac acg gcc ctg gca cga tgg ctc cct cca gtc tat gag gac ggc ttc 639
Asn Thr Ala Leu Ala Arg Trp Leu Pro Pro Val Tyr Glu Asp Gly Phe

170	175	180	185	
agt cag ccc cga ggc tgg aac ccc ggc ttc ttg tac aac ggg ttc cca				687
Ser Gln Pro Arg Gly Trp Asn Pro Gly Phe Leu Tyr Asn Gly Phe Pro	190	195	200	
ctg ccc ccg gtc cgg gag gtg aca aga cat gtc att caa gtt tca aat				735
Leu Pro Pro Val Arg Glu Val Thr Arg His Val Ile Gln Val Ser Asn	205	210	215	
gag gtt gtc aca gat gat gac cgc tat tct gac ctc ctg atg gca tgg				793
Glu Val Val Thr Asp Asp Asp Arg Tyr Ser Asp Leu Leu Met Ala Trp	220	225	230	
gga caa tac atc gac cac gac atc gcg ttc aca cca cag agc acc agc				831
Gly Gln Tyr Ile Asp His Asp Ile Ala Phe Thr Pro Gln Ser Thr Ser	235	240	245	
aaa gct gcc ttc ggg gga ggg tct gac tgc cag atg act tgt gag aac				879
Lys Ala Ala Phe Gly Gly Gly Ser Asp Cys Gln Met Thr Cys Glu Asn	250	255	260	265
caa aac cca tgt ttt ccc ata caa ctc ccg gag gag gcc cgg ccg gcc				927
Gln Asn Pro Cys Phe Pro Ile Gln Leu Pro Glu Glu Ala Arg Pro Ala	270	275	280	
gcg ggc acc gcc tgt ctg ccc ttc tac cgc tct tcg gcc gcc tgc ggc				975
Ala Gly Thr Ala Cys Leu Pro Phe Tyr Arg Ser Ser Ala Ala Cys Gly	285	290	295	
acc ggg gac caa ggc gcg ctc ttt ggg aac ctg tcc acg gcc aac ccg				1023
Thr Gly Asp Gln Gly Ala Leu Phe Gly Asn Leu Ser Thr Ala Asn Pro	300	305	310	
agg cag cag atg aac ggg ttg acc tcg ttc ctg gac gcg tcc acc gag				1071
Arg Gln Gln Met Asn Gly Leu Thr Ser Phe Leu Asp Ala Ser Thr Val	315	320	325	
tat ggc agc tcc ccg gcc cta gag agg cag ctg cgg aac tgg acc agt				1119
Tyr Gly Ser Ser Pro Ala Leu Glu Arg Gln Leu Arg Asn Trp Thr Ser	330	335	340	345
gcc gaa ggg ctg ctc cgc gtc cac ggc cgc ctc cgg gac tcc ggc cgc				1167
Ala Glu Gly Leu Leu Arg Val His Gly Arg Leu Arg Asp Ser Gly Arg	350	355	360	
gcc tac ctg ccc ttc gtg ccg cca cgc gcg cct gcg gcc tgt gcg ccc				1215
Ala Tyr Leu Pro Phe Val Pro Pro Arg Ala Pro Ala Ala Cys Ala Pro	365	370	375	
gag ccc ggc aac ccc gga gag acc cgc ggg ccc tgc ttc ctg gcc gga				1263
Glu Pro Gly Asn Pro Gly Glu Thr Arg Gly Pro Cys Phe Leu Ala Gly	380	385	390	
gac ggc cgc gcc agc gag gtc ccc tcc ctg acg gca ctg cac acg ctg				1311
Asp Gly Arg Ala Ser Glu Val Pro Ser Leu Thr Ala Leu His Thr Leu	395	400	405	

tgg ctg cgc gag cac aac cgc ctg gcc gcg gcg ctc aag gcc ctc aat	1359
Trp Leu Arg Glu His Asn Arg Leu Ala Ala Ala Leu Lys Ala Leu Asn	
410 415 420 425	
gcg cac tgg agc gcg gac gcc gtg tac cag gag gcg cgc aag gtc gtg	1407
Ala His Trp Ser Ala Asp Ala Val Tyr Gln Glu Ala Arg Lys Val Val	
430 435 440	
ggc gct ctg cac cag atc atc acc ctg agg gat tac atc ccc agg atc	1455
Gly Ala Leu His Gln Ile Ile Thr Leu Arg Asp Tyr Ile Pro Arg Ile	
445 450 455	
ctg gga ccc gag gcc ttc cag cag tac gtg ggt ccc tat gaa ggc tat	1503
Leu Gly Pro Glu Ala Phe Gln Gln Tyr Val Gly Pro Tyr Glu Gly Tyr	
460 465 470	
gac tcc acc gcc aac ccc act gtg tcc aac gtg ttc tcc aca gcc gcc	1551
Asp Ser Thr Ala Asn Pro Thr Val Ser Asn Val Phe Ser Thr Ala Ala	
475 480 485	
ttc cgc ttc ggc cat gcc acg atc cac ccg ctg gtg agg agg ctg gac	1599
Phe Arg Phe Gly His Ala Thr Ile His Pro Leu Val Arg Arg Leu Asp	
490 495 500 505	
gcc agc ttc cag gag cac ccc gac ctg ccc ggg ctg tgg ctg cac cag	1647
Ala Ser Phe Gln Glu His Pro Asp Leu Pro Gly Leu Trp Leu His Gln	
510 515 520	
gct ttc ttc agc cca tgg aca tta ctc cgt gga ggt ggt ttg gac cca	1695
Ala Phe Phe Ser Pro Trp Thr Leu Leu Arg Gly Gly Gly Leu Asp Pro	
525 530 535	
cta ata cga ggc ctt ctt gca aga cca gcc aaa ctg cag gtg cag gat	1743
Leu Ile Arg Gly Leu Leu Ala Arg Pro Ala Lys Leu Gln Val Gln Asp	
540 545 550	
cag ctg atg aac gag gag ctg acg gaa agg ctc ttt gtg ctg tcc aat	1791
Gln Leu Met Asn Glu Glu Thr Glu Arg Leu Phe Val Leu Ser Asn	
555 560 565	
tcc agc acc ttg gat ctg gcg tcc atc aac ctg cag agg ggc cgg gac	1839
Ser Ser Thr Leu Asp Leu Ala Ser Ile Asn Leu Gln Arg Gly Arg Asp	
570 575 580 585	
cac ggg ctg cca ggt tac aat gag tgg agg gag ttc tgc ggc ctg cct	1887
His Gly Leu Pro Gly Tyr Asn Glu Trp Arg Glu Phe Cys Gly Leu Pro	
590 595 600	
cgc ctg gag acc ccc gct gac ctg agc aca gcc atc gcc agc agg agc	1935
Arg Leu Glu Thr Pro Ala Asp Leu Ser Thr Ala Ile Ala Ser Arg Ser	
605 610 615	
gtg gcc gac aag atc ctg gac ttg tac aag cat cct gac aac atc gat	1983
Val Ala Asp Lys Ile Leu Asp Leu Tyr Lys His Pro Asp Asn Ile Asp	
620 625 630	

gtc tgg ctg gga ggc tta gct gaa aac ttc ctc ccc agg gct cgg aca Val Trp Leu Gly Gly Leu Ala Glu Asn Phe Leu Pro Arg Ala Arg Thr 635 640 645	2031
ggg ccc ctg ttt gcc tgt ctc att ggg aag cag atg aag gct ctg cgg Gly Pro Leu Phe Ala Cys Leu Ile Gly Lys Gln Met Lys Ala Leu Arg 650 655 660 665	2079
gac ggt gac tgg ttt tgg tgg gag aac agc cac gtc ttc acg gat gca Asp Gly Asp Trp Phe Trp Trp Glu Asn Ser His Val Phe Thr Asp Ala 670 675 680	2127
cag agg cgt gag ctg gag aag cac tcc ctg tct cgg gtc atc tgt gac Gln Arg Arg Glu Leu Glu Lys His Ser Leu Ser Arg Val Ile Cys Asp 685 690 695	2175
aac act ggc ctc acc agg gtg ccc atg gat gcc ttc caa gtc ggc aaa Asn Thr Gly Leu Thr Arg Val Pro Met Asp Ala Phe Gln Val Gly Lys 700 705 710	2223
ttc ccc gaa gac ttt gag tct tgt gac agc atc act ggc atg aac ctg Phe Pro Glu Asp Phe Glu Ser Cys Asp Ser Ile Thr Gly Met Asn Leu 715 720 725	2271
gag gcc tgg agg gaa acc ttt cct caa gac gac aag tgt ggc ttc cca Glu Ala Trp Arg Glu Thr Phe Pro Gln Asp Asp Lys Cys Gly Phe Pro 730 735 740 745	2319
gag agc gtg gag aat ggg gac ttt gtg cac tgt gag gag tct ggg agg Glu Ser Val Glu Asn Gly Asp Phe Val His Cys Glu Glu Ser Gly Arg 750 755 760	2367
cgc gtg ctg gtg tat tcc tgc cgg cac ggg tat gag ctc caa ggc cgg Arg Val Leu Val Tyr Ser Cys Arg His Gly Tyr Glu Leu Gln Gly Arg 765 770 775	2415
gag cag ctc act tgc acc cag gaa gga tgg gat ttc cag cct ccc ctc Glu Gln Leu Thr Cys Thr Gln Glu Gly Trp Asp Phe Gln Pro Pro Leu 780 785 790	2463
tgc aaa gat gtg aac gag tgt gca gac ggt gcc cac ccc ccc tgc cac Cys Lys Asp Val Asn Glu Cys Ala Asp Gly Ala His Pro Pro Cys His 795 800 805	2511
gcc tct gcg agg tgc aga aac acc aaa ggc ggc ttc cag tgt ctc tgc Ala Ser Ala Arg Cys Arg Asn Thr Lys Gly Gly Phe Gln Cys Leu Cys 810 815 820 825	2559
gcg gac ccc tac gag tta gga gac gat ggg aga acc tgc gta gac tcc Ala Asp Pro Tyr Glu Leu Gly Asp Asp Gly Arg Thr Cys Val Asp Ser 830 835 840	2607
ggg agg ctc cct cgg gtg act tgg atc tcc atg tcg ctg gct gct ctg Gly Arg Leu Pro Arg Val Thr Trp Ile Ser Met Ser Leu Ala Ala Leu 845 850 855	2655
ctg atc gga ggc ttc gca ggt ctc acc tcg acg gtg att tgc agg tgg	2703

Leu Ile Gly Gly Phe Ala Gly Leu Thr Ser Thr Val Ile Cys Arg Trp
860 865 870

aca cgc act ggc act aaa tcc aca ctg ccc atc tcg gag aca ggc gga 2751
Thr Arg Thr Gly Thr Lys Ser Thr Leu Pro Ile Ser Glu Thr Gly Gly
875 880 885

gga act ccc gag ctg aga tgc gga aag cac cag gcc gta ggg acc tca 2799
Gly Thr Pro Glu Leu Arg Cys Gly Lys His Gln Ala Val Gly Thr Ser
890 895 900 905

ccg cag cgg gcc gca gct cag gac tcg gag cag gag agt gct ggg atg 2847
Pro Gln Arg Ala Ala Ala Gln Asp Ser Glu Gln Glu Ser Ala Gly Met
910 915 920

gaa ggc cgg gat act cac agg ctg ccg aga gcc ctc tgagggcaaa 2893
Glu Gly Arg Asp Thr His Arg Leu Pro Arg Ala Leu
925 930

gtggcaggac actgcagaac agcttcatgt tcccaaaatc accgtacgac tcttttccaa 2953

acacaggcaa atcggaaatc agcaggacga ctgttttccc aacacgggta aatctagtac 3013

catgtcgtag ttactctcag gcatggatga ataaatgtta tagctgcaaa aaaaaaaaaa 3072

<210> 3
<211> 933
<212> PRT
<213> Homo sapiens
<400> 3

Met Arg Ala Leu Ala Val Leu Ser Val Thr Leu Val Met Ala Cys Thr
1 5 10 15

Glu Ala Phe Phe Pro Phe Ile Ser Arg Gly Lys Glu Leu Leu Trp Gly
20 25 30

Lys Pro Glu Glu Ser Arg Val Ser Ser Val Leu Glu Glu Ser Lys Arg
35 40 45

Leu Val Asp Thr Ala Met Tyr Ala Thr Met Gln Arg Asn Leu Lys Lys
50 55 60

Arg Gly Ile Leu Ser Gly Ala Gln Leu Leu Ser Phe Ser Lys Leu Pro
65 70 75 80

Glu Pro Thr Ser Gly Val Ile Ala Arg Ala Ala Glu Ile Met Glu Thr
85 90 95

Ser Ile Gln Ala Met Lys Arg Lys Val Asn Leu Lys Thr Gln Gln Ser
100 105 110

Gln His Pro Thr Asp Ala Leu Ser Glu Asp Leu Leu Ser Ile Ile Ala
115 120 125

Asn Met Ser Gly Cys Leu Pro Tyr Met Leu Pro Pro Lys Cys Pro Asn
130 135 140

Thr Cys Leu Ala Asn Lys Tyr Arg Pro Ile Thr Gly Ala Cys Asn Asn
145 150 155 160

Arg Asp His Pro Arg Trp Gly Ala Ser Asn Thr Ala Leu Ala Arg Trp
165 170 175

Leu Pro Pro Val Tyr Glu Asp Gly Phe Ser Gln Pro Arg Gly Trp Asn
180 185 190

Pro Gly Phe Leu Tyr Asn Gly Phe Pro Leu Pro Pro Val Arg Glu Val
195 200 205

Thr Arg His Val Ile Gln Val Ser Asn Glu Val Val Thr Asp Asp Asp
210 215 220

Arg Tyr Ser Asp Leu Leu Met Ala Trp Gly Gln Tyr Ile Asp His Asp
225 230 235 240

Ile Ala Phe Thr Pro Gln Ser Thr Ser Lys Ala Ala Phe Gly Gly Gly
245 250 255

Ser Asp Cys Gln Met Thr Cys Glu Asn Gln Asn Pro Cys Phe Pro Ile
260 265 270

Gln Leu Pro Glu Glu Ala Arg Pro Ala Ala Gly Thr Ala Cys Leu Pro
275 280 285

Phe Tyr Arg Ser Ser Ala Ala Cys Gly Thr Gly Asp Gln Gly Ala Leu
290 295 300

Phe Gly Asn Leu Ser Thr Ala Asn Pro Arg Gln Gln Met Asn Gly Leu
305 310 315 320

Thr Ser Phe Leu Asp Ala Ser Thr Val Tyr Gly Ser Ser Pro Ala Leu

325

330

335

Glu Arg Gln Leu Arg Asn Trp Thr Ser Ala Glu Gly Leu Leu Arg Val
 340 345 350

His Gly Arg Leu Arg Asp Ser Gly Arg Ala Tyr Leu Pro Phe Val Pro
 355 360 365

Pro Arg Ala Pro Ala Ala Cys Ala Pro Glu Pro Gly Asn Pro Gly Glu
 370 375 380

Thr Arg Gly Pro Cys Phe Leu Ala Gly Asp Gly Arg Ala Ser Glu Val
 385 390 395 400

Pro Ser Leu Thr Ala Leu His Thr Leu Trp Leu Arg Glu His Asn Arg
 405 410 415

Leu Ala Ala Ala Leu Lys Ala Leu Asn Ala His Trp Ser Ala Asp Ala
 420 425 430

Val Tyr Gln Glu Ala Arg Lys Val Val Gly Ala Leu His Gln Ile Ile
 435 440 445

Thr Leu Arg Asp Tyr Ile Pro Arg Ile Leu Gly Pro Glu Ala Phe Gln
 450 455 460

Gln Tyr Val Gly Pro Tyr Glu Gly Tyr Asp Ser Thr Ala Asn Pro Thr
 465 470 475 480

Val Ser Asn Val Phe Ser Thr Ala Ala Phe Arg Phe Gly His Ala Thr
 485 490 495

Ile His Pro Leu Val Arg Arg Leu Asp Ala Ser Phe Gln Glu His Pro
 500 505 510

Asp Leu Pro Gly Leu Trp Leu His Gln Ala Phe Phe Ser Pro Trp Thr
 515 520 525

Leu Leu Arg Gly Gly Gly Leu Asp Pro Leu Ile Arg Gly Leu Leu Ala
 530 535 540

Arg Pro Ala Lys Leu Gln Val Gln Asp Gln Leu Met Asn Glu Glu Leu
 545 550 555 560

Thr	Glu	Arg	Leu	Phe	Val	Leu	Ser	Asn	Ser	Ser	Thr	Leu	Asp	Leu	Ala	565	570	575	
Ser	Ile	Asn	Leu	Gln	Arg	Gly	Arg	Asp	His	Gly	Leu	Pro	Gly	Tyr	Asn	580	585	590	
Glu	Trp	Arg	Glu	Phe	Cys	Gly	Leu	Pro	Arg	Leu	Glu	Thr	Pro	Ala	Asp	595	600	605	
Leu	Ser	Thr	Ala	Ile	Ala	Ser	Arg	Ser	Val	Ala	Asp	Lys	Ile	Leu	Asp	610	615	620	
Leu	Tyr	Lys	His	Pro	Asp	Asn	Ile	Asp	Val	Trp	Leu	Gly	Gly	Leu	Ala	625	630	635	640
Glu	Asn	Phe	Leu	Pro	Arg	Ala	Arg	Thr	Gly	Pro	Leu	Phe	Ala	Cys	Leu	645	650	655	
Ile	Gly	Lys	Gln	Met	Lys	Ala	Leu	Arg	Asp	Gly	Asp	Trp	Phe	Trp	Trp	660	665	670	
Glu	Asn	Ser	His	Val	Phe	Thr	Asp	Ala	Gln	Arg	Arg	Glu	Leu	Glu	Lys	675	680	685	
His	Ser	Leu	Ser	Arg	Val	Ile	Cys	Asp	Asn	Thr	Gly	Leu	Thr	Arg	Val	690	695	700	
Pro	Met	Asp	Ala	Phe	Gln	Val	Gly	Lys	Phe	Pro	Glu	Asp	Phe	Glu	Ser	705	710	715	720
Cys	Asp	Ser	Ile	Thr	Gly	Met	Asn	Leu	Glu	Ala	Trp	Arg	Glu	Thr	Phe	725	730	735	
Pro	Gln	Asp	Asp	Lys	Cys	Gly	Phe	Pro	Glu	Ser	Val	Glu	Asn	Gly	Asp	740	745	750	
Phe	Val	His	Cys	Glu	Glu	Ser	Gly	Arg	Arg	Val	Leu	Val	Tyr	Ser	Cys	755	760	765	
Arg	His	Gly	Tyr	Glu	Leu	Gln	Gly	Arg	Glu	Gln	Leu	Thr	Cys	Thr	Gln	770	775	780	

Glu Gly Trp Asp Phe Gln Pro Pro Leu Cys Lys Asp Val Asn Glu Cys
 785 790 795 800

Ala Asp Gly Ala His Pro Pro Cys His Ala Ser Ala Arg Cys Arg Asn
 805 810 815

Thr Lys Gly Gly Phe Gln Cys Leu Cys Ala Asp Pro Tyr Glu Leu Gly
 820 825 830

Asp Asp Gly Arg Thr Cys Val Asp Ser Gly Arg Leu Pro Arg Val Thr
 835 840 845

Trp Ile Ser Met Ser Leu Ala Ala Leu Leu Ile Gly Gly Phe Ala Gly
 850 855 860

Leu Thr Ser Thr Val Ile Cys Arg Trp Thr Arg Thr Gly Thr Lys Ser
 865 870 875 880

Thr Leu Pro Ile Ser Glu Thr Gly Gly Gly Thr Pro Glu Leu Arg Cys
 885 890 895

Gly Lys His Gln Ala Val Gly Thr Ser Pro Gln Arg Ala Ala Ala Gln
 900 905 910

Asp Ser Glu Gln Glu Ser Ala Gly Met Glu Gly Arg Asp Thr His Arg
 915 920 925

Leu Pro Arg Ala Leu
 930

<210> 4
 <211> 45
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(45)
 <223>

<400> 4
 aac cca tgt ttt ccc ata caa ctc ccg gag gag gcc cgg ccg gcc
 Asn Pro Cys Phe Pro Ile Gln Leu Pro Glu Glu Ala Arg Pro Ala
 1 5 10 15

<210> 5
<211> 15
<212> PRT
<213> Homo sapiens

<400> 5

Asn	Pro	Cys	Phe	Pro	Ile	Gln	Leu	Pro	Glu	Glu	Ala	Arg	Pro	Ala
1				5					10					15

<210> 6
<211> 29
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (3)..(29)
<223>

<400> 6
gc aaa ttc ccc gaa gac ttt gag tct tgt
Lys Phe Pro Glu Asp Phe Glu Ser Cys
1 5

29

<210> 7
<211> 9
<212> PRT
<213> Homo sapiens

<400> 7

Lys	Phe	Pro	Glu	Asp	Phe	Glu	Ser	Cys
1				5				

<210> 8
<211> 52
<212> DNA
<213> Artificial Sequence

<220>
<223> A mutagenic primer to a human thyrodine peroxidase cDNA designed to generate two stop codons at nucleotides 2629-2631 and 2641-2643.

<400> 8
aggctccctc gggtgacttg aattcccatg tagctggctg ctctgctgat cg

52

<210> 9
<211> 14
<212> DNA

<213> Artificial Sequence

<220>

<223> An EcoRI linker.

<400> 9

gaattcggca cgag

14

<210> 10

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Human thyrodine peroxidase primer.

<400> 10

ggttacaatg agtggaggga gt

22

<210> 11

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Human thyrodine peroxidase primer.

<400> 11

gtggctgttc tcccacaaa ac

22

<210> 12

<211> 47

<212> DNA

<213> Homo sapiens

<400> 12

aaaacccatg ttttcccata caactcccgg aggaggcccg gccggcc

47

SEQUENCE LISTING

<110> Rapoport, Basil

<120> Disease Associated Human Autoantibodies Specific For
Human Thyroid Peroxidase.

<130> 08/482,402

<140> 08/482,402

<141> 1995-06-07

<150> PCT/US92/06283

<151> 1992-07-30

<150> 07/750,579

<151> 1991-08-28

<150> 07/738,040

<151> 1991-07-30

<150> 07/559,955

<151> 1990-07-31

<150> 07/472,070

<151> 1990-01-30

<150> 07/388,044

<151> 1989-07-31

<150> 08/196,082

<151> 1994-03-03

<150> 08/182,117

<151> 1994-01-27

<150> PCT US92/07381

<151> 1992-08-28

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 104

<212> DNA

<213> human

<220>

<223> See Brief Description of the Drawings fig 6 of
Application for detail

<400> 1

aggctccctc gggtgacttg gatctccatg tcgctggctg ctctgctgat cgaggctccc
60
tcgggtgact tgaattccca tgtagctggc tgctctgctg atcg
104

<210> 2

<211> 3072

<212> DNA

<213> human

<220>

<223> See Brief Description of the Drawing figure 7 of
application for detail

<400> 2

gaggcaattg aggcgcccac ttcagaagag ttacagccgt gaaaattact cagcagtgca
60
gttggtgag aagaggaaaa aagaatgaga gcgctggctg tgctgtctgt cacgctgggt
120
atggcctgca cagaagcctt cttcccttc atctcgagag ggaaagaact cctttgggga
180
aagcctgagg agtctcgtgt ctctagcgtc ttggaggaaa gcaagcgctt ggtggacacc
240
gccatgtacg ccacgatgca gagaaacctc aagaaaagag gaatcctttc tggagctcag
300
cttctgtctt tttccaaact tcctgagcca acaagcggag tgattgcccg agcagcagag
360
ataatggaaa catcaatata agcgatgaaa agaaaagtca acctgaaaac tcaacaatca
420
cagcatccaa cggatgcttt atcagaagat ctgctgagca tcattgcaaa catgtctgga
480
tgtctccctt acatgctgcc cccaaaatgc ccaaactt gcctggcgaa caaatacagg
540
cccatcacag gagcttgcaa caacagagac caccacagat ggggagcctc caacacggcc
600
ctggcacgat ggctccctcc agtctatgag gacggcttca gtcagccccg aggctggaac
660
cccggttct tgtacaacgg gttccactg ccccggtcc gggaggtgac aagacatgtc
720
attcaagttt caaatgaggt tgtcacagat gatgaccgct attctgacct cctgatggca
780

tggggacaat acatcgacca cgacatcgcg ttcacaccac agagcaccag caaagctgcc
 840
 ttcgggggag ggtctgactg ccagatgact tgtgagaacc aaaacccatg ttttcccata
 900
 caactcccgg aggaggcccg gccggccgcg ggcaccgcct gtctgccctt ctaccgctct
 960
 tcggccgcct gcggcaccgg ggaccaaggc gcgctctttg ggaacctgtc cacggccaac
 1020
 ccgaggcagc agatgaacgg gttgacctcg ttcttgagcg cgtccaccgt gtatggcagc
 1080
 tccccggccc tagagaggca gctgcggaac tggaccagtg ccgaagggtc gctccgcgtc
 1140
 cacggccgccc tccgggactc cggccgcgccc tacctgccct tcgtgccgccc acgcgcgcct
 1200
 gcggcctgtg cgcccagacc cggcaacccc ggagagaccc gcggggccctg cttcctggcc
 1260
 ggagacggcc gcgccagcga ggtcccctcc ctgacggcac tgcacacgct gtggctgcgc
 1320
 gagcacaacc gcctggccgc ggcgctcaag gccctcaatg cgcactggag cgcggaacgc
 1380
 gtgtaccagg aggcgcgcaa ggtcgtgggc gctctgcacc agatcatcac cctgagggat
 1440
 tacatcccca ggatcctggg acccgaggcc ttccagcagt acgtgggtcc ctatgaaggc
 1500
 tatgactcca ccgccaaccc cactgtgtcc aacgtgttct ccacagccgc cttccgcttc
 1560
 ggccatgcca cgatccaccc gctggtgagg aggctggacg ccagcttcca ggagcacccc
 1620
 gacctgcccg ggctgtggct gcaccaggct ttcttcagcc catggacatt actccgtgga
 1680
 ggtggtttgg acccactaat acgaggcctt cttgcaagac cagccaaact gcagggtgcag
 1740
 gatcagctga tgaacgagga gctgacggaa aggctctttg tgctgtccaa ttccagcacc
 1800
 ttggatctgg cgtccatcaa cctgcagagg ggccgggacc acgggctgcc aggttacaat
 1860
 gagtggaggg agttctgcgg cctgcctcgc ctggagaccc ccgctgacct gagcacagcc
 1920
 atcgccagca ggagcgtggc cgacaagatc ctggacttgt acaagcatcc tgacaacatc
 1980
 gatgtctggc tgggaggctt agctgaaaac ttctcccca gggctcggac agggcccctg
 2040
 tttgcctgtc tcattgggaa gcagatgaag gctctgcggg acggtgactg gttttggtgg
 2100
 gagaacagcc acgtcttcac ggatgcacag aggcgtgagc tggagaagca ctccctgtct
 2160
 cgggtcatct gtgacaacac tggcctcacc agggtgccca tggatgcctt ccaagtcggc
 2220

aaattccccg aagactttga gtcttgtgac agcatcactg gcatgaacct ggaggcctgg
 2280
 agggaaacct ttcctcaaga cgacaggtgt ggcttcccag agagcgtgga gaatggggac
 2340
 tttgtgcact gtgaggagtc tgggaggcgc gtgctggtgt attcctgccg gcacgggtat
 2400
 gagctccaag gccgggagca gctcacttgc acccaggaag gatgggattt ccagcctccc
 2460
 ctctgcaaag atgtgaacga gtgtgcagac ggtgcccacc cccctgccca cgctgtgcg
 2520
 aggtgcagaa acaccaaagg cggcttccag tgtctctgcg cggaccccta cgagtttaga
 2580
 gacgatggga gaacctgcgt agactccggg aggctccctc gggtgacttg gatctccatg
 2640
 tcgctggctg ctctgctgat cggaggcttc gcaggctctca cctcgacggt gatttgcagg
 2700
 tggacacgca ctggcactaa atccacactg cccatctcgg agacaggcgg aggaactccc
 2760
 gagctgagat gcggaaagca ccaggccgta gggacctcac cgcagcgggc cgcagctcag
 2820
 gactcggagc aggagagtgc tgggatggaa ggccgggata ctcacaggct gccgagagcc
 2880
 ctctgagggc aaagtggcag gacactgcag aacagcttca tggtcccaaa atcacgttac
 2940
 gactcttttc caaacacagg caaatcggaa atcagcagga cgactgtttt cccaacacgg
 3000
 gtaaatctag taccatgtcg tagttactct caggcatgga tgaataaatg ttatagctgc
 3060
 aaaaaaaaaa aa
 3072

<210> 3
 <211> 45
 <212> DNA
 <213> human

<220>

<223> See Brief Description of the Drawings figure 18 of the Application for details

<400> 3

aacccatgtt ttccataca actcccggag gaggcccggc cggcc
 45

<210> 4
 <211> 29

<212> DNA
<213> human

<220>

<223> See Brief Description of the Drawing fig 19 of the
Applicaion for details

<400> 4

gcaaattccc cgaagacttt gagtcttgt
29